

SEQUENCE LISTING

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Hutchison, Michele
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<120> TAO PROTEIN KINASE POLYPEPTIDES AND
METHODS OF USE THEREFOR

<130> 860098.421C1

<150> .09/060,410

<151> 1998-04-14

<160> 28

<170> FastSEQ for Windows Version 4.0

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<213> Rattus norvegicus

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atg cca tca act aac aga gca ggc agt cta aag gac cct gaa atc gca	168
Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala	
1 5 10 15	
gag ctc ttc ttc aaa gaa gat ccg gaa aaa ctc ttc aca gat ctc aga	216
Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg	
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gaa atc ggc cat ggg agc ttt gga gca gtt tat ttt gca cga gat gtg	264
Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val	
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cgt act aat gaa gtg gtg gcc atc aag aaa atg tct tat agt gga aag	312
Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys	
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cag tct act gag aaa tgg cag gat att att aag gaa gtc aag ttt cta	360
Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu	
65 70 75 80	
caa aga ata aaa cat ccc aac agt ata gaa tac aaa ggc tgc tat tta	408
Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu	
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cgt gaa cac aca gca tgg ctt gta atg gaa tat tgt tta gga tct gct	456
Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala	

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70410

41

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gca gca att aca cat ggt gct Ala Ala Ile Thr His Gly 130	ctc cag gga tta gct tat Ala Leu Gln Gly Leu Ala Tyr 135 140	tta cat tct Leu His Ser 140	552
cat acc atg atc cat aga gat His Thr Met Ile His Arg Asp 145	atc aaa gca gga aat atc Ile Lys Ala Gly Asn Ile 150 155	ctt ctg aca Leu Leu Thr 160	600
gaa cca ggc caa gtg aaa ctt Glu Pro Gly Gln Val Lys Leu 165	gct gac ttt gga tct gct Ala Asp Phe Gly Ser Ala 170	tcc atg gcc Ser Met Ala 175	648
tcc cct gcc aat tct ttt gtg Ser Pro Ala Asn Ser Phe Val 180	gga aca cca tat tgg atg Gly Thr Pro Tyr Trp Met 185	gcc cca gaa Ala Pro Glu 190	696
gta att tta gcc atg gat gaa Val Ile Leu Ala Met Asp Glu 195	gga cca tat gat ggc aaa Gly Gln Tyr Asp Gly Lys 200 205	gtt gat gta Val Asp Val 205	744
tgg tct ctt gga ata aca tgt Trp Ser Leu Gly Ile Thr Cys 210	att gaa tta gcc gag agg Ile Glu Leu Ala Glu Arg 215 220	aag cct cct Lys Pro Pro 220	792
tta ttt aat atg aat gca atg Leu Phe Asn Met Asn Ala Met 225	agt gcc tta tat cac ata Ser Ala Leu Tyr His Ile 230 235	gcc caa aat Ala Gln Asn 240	840
gaa tcc cct aca cta cag tct Glu Ser Pro Thr Leu Gln Ser 245	aat gaa tgg tct gat tat Asn Glu Trp Ser Asp Tyr 250	ttt cga aac Phe Arg Asn 255	888
ttt gta gat tct tgc ctc cag Phe Val Asp Ser Cys Leu Gln 260	aaa atc cct caa gat cgc Lys Ile Pro Gln Asp Arg 265	cct aca tca Pro Thr Ser 270	936
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gtg tta ata gat ctt att caa Val Leu Ile Asp Leu Ile Gln 290	agg aca aag gat gca gta Arg Thr Lys Asp Ala Val 295 300	aga gag ctg Arg Glu Leu 300	1032
gac aat cta caa tat cga aag Asp Asn Leu Gln Tyr Arg Lys 305	atg aag aaa ctc ctt ttc Met Lys Lys Leu Leu Phe 310 315	cag gag gca Gln Glu Ala 320	1080
cat aat gga cca gca gta gaa His Asn Gly Pro Ala Val Glu 325	gca cag gaa gaa gag gag Ala Gln Glu Glu Glu Glu 330	gag caa gat Gln Asp 335	1128

43

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ggt cgg cat aac ttg gaa cag gac ctt gtc agg gag gag tta aac aaa Gly Arg His Asn Leu Glu Gln Asp Leu Val Arg Glu Glu Leu Asn Lys 625 630 635 640			2040
agg cag act cag aag gac tta gaa cat gca atg tta ctg cga cag cat Arg Gln Thr Gln Lys Asp Leu Glu His Ala Met Leu Leu Arg Gln His 645 650 655			2088
gaa tcc atg caa gaa ctg gag ttt cgc cac ctc aac act att cag aag Glu Ser Met Gln Glu Leu Glu Phe Arg His Leu Asn Thr Ile Gln Lys 660 665 670			2136
atg cgc tgt gag ttg atc aga ctg caa cat caa act gag ctt act aac Met Arg Cys Glu Leu Ile Arg Leu Gln His Gln Thr Glu Leu Thr Asn 675 680 685			2184
cag ctg gaa tac aat aag aga agg gaa cgg gaa cta aga cgg aaa cat Gln Leu Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu Arg Arg Lys His 690 695 700			2232
gtc atg gaa gtt cga cag cag cct aag agt ttg aag tct aaa gaa ctc Val Met Glu Val Arg Gln Gln Pro Lys Ser Leu Lys Ser Lys Glu Leu 705 710 715 720			2280
caa ata aaa aag cag ttt cag gat acc tgc aaa att caa acc aga cag Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Ile Gln Thr Arg Gln 725 730 735			2328
tac aaa gca tta agg aat cac cta ctg gag act aca cca aag agt gag Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys Ser Glu 740 745 750			2376
cac aaa gct gtt ctg aaa aga ctc aag gag gaa cag act cgg aag tta His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg Lys Leu 755 760 765			2424
gcc atc ttg gct gag cag tat gat cat agc att aat gaa atg ctc tcc Ala Ile Leu Ala Glu Gln Tyr Asp His Ser Ile Asn Glu Met Leu Ser 770 775 780			2472
aca caa gct ctg cgt ttg gat gaa gca cag gaa gca gaa tgc cag gtt Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Val 785 790 795 800			2520

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agc aaa atc aag atg cag gct gag gcc caa cat gat cga gag ctt cga	2616
Ser Lys Ile Lys Met Gln Ala Glu Ala Gln His Asp Arg Glu Leu Arg	
820 825 830	
gag ctg gaa caa agg gtc tcc ctt cgg aga gca ctc tta gaa cag aag	2664
Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu Leu Glu Gln Lys	
835 840 845	
att gaa gaa gag atg ttg gct ttg cag aat gaa cgc aca gaa cga ata	2712
Ile Glu Glu Glu Met Leu Ala Leu Gln Asn Glu Arg Thr Glu Arg Ile	
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Arg Ser Leu Leu Glu Arg Gln Ala Arg Glu Ile Glu Ala Phe Asp Ser	
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Glu Ser Met Arg Leu Gly Phe Ser Asn Met Val Leu Ser Asn Leu Ser	
885 890 895	
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Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His	
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Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly	
915 920 925	
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Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp	
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ggt cac ccc tca ggg cca atg caa ggg gta cct cga ggt agc agt ata	3000
Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile	
945 950 955 960	
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Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly	
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Ser Asn Gly Ser His Met Ser Tyr Thr	
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45

<212> PRT

<213> Rattus norvegicus

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Glu	Ile	Gly	His	Gly	Ser	Phe	Gly	Ala	Val	Tyr	Phe	Ala	Arg	Asp	Val
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Arg	Thr	Asn	Glu	Val	Val	Ala	Ile	Lys	Lys	Met	Ser	Tyr	Ser	Gly	Lys
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Gln	Arg	Ile	Lys	His	Pro	Asn	Ser	Ile	Glu	Tyr	Lys	Gly	Cys	Tyr	Leu
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Ser	Asp	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	
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Ala	Ala	Ile	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	Tyr	Leu	His	Ser
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Glu	Pro	Gly	Gln	Val	Lys	Leu	Ala	Asp	Phe	Gly	Ser	Ala	Ser	Met	Ala
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Ser	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu
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Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Val
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Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro
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Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn
225					230					235					240
Glu	Ser	Pro	Thr	Leu	Gln	Ser	Asn	Glu	Trp	Ser	Asp	Tyr	Phe	Arg	Asn
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Val	Leu	Ile	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu
	290					295					300				
Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Leu	Leu	Phe	Gln	Glu	Ala
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His	Asn	Gly	Pro	Ala	Val	Glu	Ala	Gln	Glu	Glu	Glu	Glu	Glu	Gln	Asp
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His	Gly	Gly	Gly	Arg	Thr	Gly	Thr	Val	Asn	Ser	Val	Gly	Ser	Asn	Gln
			340					345					350		
Ser	Ile	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ser	Ser	Val
		355					360					365			
Asn	Ser	Leu	Pro	Asp	Ala	Ser	Asp	Asp	Lys	Ser	Glu	Leu	Asp	Met	Met
	370					375					380				
Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn	Ser	Ser	Val	Ile	His	Leu	Lys
385					390						395				400
Pro	Glu	Glu	Glu	Asn	Tyr	Gln	Glu	Glu	Gly	Asp	Pro	Arg	Thr	Arg	Ala
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Ser	Ala	Pro	Gln	Ser	Pro	Pro	Gln	Val	Ser	Arg	His	Lys	Ser	His	Tyr
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47

Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His
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 Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly
 915 920 925
 Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp
 930 935 940
 Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile
 945 950 955 960
 Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly
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 ccagggggcca tc atg cca gct ggg ggc cgg gcc ggg agc ctg aag gac cct 231
 Met Pro Ala Gly Gly Arg Ala Gly Ser Leu Lys Asp Pro
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 gat gta gct gag ctc ttc ttc aaa gat gac cct gag aag ctt ttc tct 279
 Asp Val Ala Glu Leu Phe Phe Lys Asp Asp Pro Glu Lys Leu Phe Ser
 15 20 25
 gac ctc cgg gaa att ggc cat ggc agt ttt gga gct gtg tac ttt gcc 327
 Asp Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala
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 cgg gat gtc cgg aac agt gag gtg gtg gcc atc aag aag atg tcc tat 375
 Arg Asp Val Arg Asn Ser Glu Val Val Ala Ile Lys Lys Met Ser Tyr
 50 55 60
 agt ggg aag caa tca aat gag aaa tgg cag gat atc atc aag gag gtg 423
 Ser Gly Lys Gln Ser Asn Glu Lys Trp Gln Asp Ile Ile Lys Glu Val
 65 70 75
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 Arg Phe Leu Gln Lys Leu Arg His Pro Asn Thr Ile Gln Tyr Arg Gly
 80 85 90
 tgt tac ctg agg gag cac aca gct tgg ctg gtg atg gag tat tgc ctg 519
 Cys Tyr Leu Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu
 95 100 105
 ggt tca gct tct gat ctt ctc gaa gtg cac aag aag ccg ctg cag gag 567
 Gly Ser Ala Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu

49

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Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser	
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Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu	
370 375 380	
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Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu	
385 390 395	
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Ser Arg Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser	
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cac agc tcc atc atc cac cgg ctg ccg ggc tca gac aac cta tat gat	1479
His Ser Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp	
415 420 425	
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Asp Pro Tyr Gln Pro Glu Met Thr Pro Gly Pro Leu Gln Pro Pro Ala	
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gcc cct ccc acc tcc acc tcc tcc tct tct gct cgc cgc aga gct tat	1575
Ala Pro Pro Thr Ser Thr Ser Ser Ser Ser Ala Arg Arg Arg Ala Tyr	
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Cys Arg Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val	
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Leu Ser Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu	
495 500 505	
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Ala Ala Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln	
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 Gln Arg Ile Leu Gly Glu Glu Met Gly Thr Phe Ser Ser Ser Pro Gln
 815 820 825

 aaa cat agg agt ctg gtt aat gag gaa gat tgg gat ata tct aaa gaa 2727
 Lys His Arg Ser Leu Val Asn Glu Glu Asp Trp Asp Ile Ser Lys Glu
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 975 980 985

 gca ctg ctg gcc ctt gag gta gga cta gtg ggc ctg ggg gcc tcc tac 3207
 Ala Leu Leu Ala Leu Glu Val Gly Leu Val Gly Leu Gly Ala Ser Tyr
 990 995 1000 1005

 ctg ttc ctt tgt aca gct cta cac ctg cca ccc agt ctg ttc tta ctc 3255
 Leu Phe Leu Cys Thr Ala Leu His Leu Pro Pro Ser Leu Phe Leu Leu
 1010 1015 1020

 ctg gct cag ggc act gca ctg ggg gct gtc ctt agc ctg agc tgg cgc 3303
 Leu Ala Gln Gly Thr Ala Leu Gly Ala Val Leu Ser Leu Ser Trp Arg
 1025 1030 1035

 aga ggc ctt atg ggt gtg cct ctg ggc ctt ggg gct gcc tgg ctc cta 3351
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53

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Glu	Ile	Gly 35	His	Gly	Ser	Phe	Gly 40	Ala	Val	Tyr	Phe	Ala 45	Arg	Asp	Val	
Arg	Asn 50	Ser	Glu	Val	Val	Ala 55	Ile	Lys	Lys	Met	Ser 60	Tyr	Ser	Gly	Lys	
Gln 65	Ser	Asn	Glu	Lys	Trp 70	Gln	Asp	Ile	Ile	Lys 75	Glu	Val	Arg	Phe	Leu 80	
Gln	Lys	Leu	Arg	His 85	Pro	Asn	Thr	Ile 90	Gln	Tyr	Arg	Gly	Cys	Tyr 95	Leu	
Arg	Glu	His	Thr 100	Ala	Trp	Leu	Val	Met 105	Glu	Tyr	Cys	Leu	Gly 110	Ser	Ala	
Ser	Asp	Leu 115	Leu	Glu	Val	His	Lys 120	Lys	Pro	Leu	Gln	Glu 125	Val	Glu	Ile	
Ala 130	Ala	Val	Thr	His	Gly	Ala 135	Leu	Gln	Gly	Leu	Ala 140	Tyr	Leu	His	Ser	
His 145	Asn	Met	Ile	His	Arg 150	Asp	Val	Lys	Ala	Gly 155	Asn	Ile	Leu	Leu	Ser 160	
Glu	Pro	Gly	Leu 165	Val	Lys	Leu	Gly	Asp	Phe 170	Gly	Ser	Ala	Ser	Ile 175	Met	
Ala	Pro	Ala	Asn 180	Ser	Phe	Val	Gly	Thr 185	Pro	Tyr	Trp	Met	Ala 190	Pro	Glu	
Val	Ile	Leu 195	Ala	Met	Asp	Glu	Gly 200	Gln	Tyr	Asp	Gly	Lys 205	Val	Asp	Val	
Trp	Ser 210	Leu	Gly	Ile	Thr	Cys 215	Ile	Glu	Leu	Ala	Glu 220	Arg	Lys	Pro	Pro	
Leu 225	Phe	Asn	Met	Asn	Ala 230	Met	Ser	Ala	Leu	Tyr 235	His	Ile	Ala	Gln	Asn 240	
Glu	Ser	Pro	Ala 245	Leu	Gln	Ser	Gly	His	Trp 250	Ser	Glu	Tyr	Phe	Arg 255	Asn	
Phe	Val	Asp	Ser 260	Cys	Leu	Gln	Lys	Ile 265	Pro	Gln	Asp	Arg	Pro 270	Thr	Ser	
Glu	Val	Leu 275	Leu	Lys	His	Arg	Phe 280	Val	Leu	Arg	Glu	Arg 285	Pro	Pro	Thr	
Val	Ile 290	Met	Asp	Leu	Ile	Gln 295	Arg	Thr	Lys	Asp	Ala 300	Val	Arg	Glu	Leu	
Asp 305	Asn	Leu	Gln	Tyr	Arg 310	Lys	Met	Lys	Lys	Ile 315	Leu	Phe	Gln	Glu	Ala 320	
Pro	Asn	Gly	Pro	Gly 325	Ala	Glu	Ala	Pro	Glu	Glu 330	Glu	Glu	Glu	Ala 335	Glu	
Pro	Tyr	Met	His 340	Arg	Ala	Gly	Thr	Leu 345	Thr	Ser	Leu	Glu	Ser 350	Ser	His	
Ser	Val	Pro 355	Ser	Met	Ser	Ile	Ser 360	Ala	Ser	Ser	Gln	Ser 365	Ser	Ser	Val	
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Glu 385	Glu	Glu	Glu	Glu	Glu 390	Glu	Glu	Glu	Glu	Gly 395	Pro	Glu	Ser	Arg	Glu	
Met	Ala	Met	Met	Gln 405	Glu	Gly	Glu	His	Thr 410	Val	Thr	Ser	His	Ser	Ser	

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			420					425					430		
Gln	Pro	Glu	Met	Thr	Pro	Gly	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro	Pro
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Thr	Ser	Thr	Ser	Ser	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg	Asn
	450					455					460				
Arg	Asp	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg	Gln
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Ile	Gln	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser	Gly
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		515					520					525			
Glu	Leu	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Thr	Glu	Ala	Glu	Lys	Leu
	530					535					540				
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545					550					555					560
Ala	Glu	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys	Lys
				565					570					575	
Glu	Leu	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu	Arg
			580					585					590		
Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro	Lys
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	610					615					620				
Cys	Gln	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln	Tyr
625					630					635					640
Phe	Glu	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	Arg
			645						650					655	
His	Ser	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	Gln
			660					665					670		
Thr	Gln	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	Ala
		675					680					685			
Thr	Arg	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg
	690					695					700				
Ala	Glu	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu
705					710					715					720
Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala
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Gln	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln	Leu
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Pro	Met	Gly	Leu	Pro	Ala	Thr	Gly	Ala	Leu	Gly	Pro	Leu	Ser	Thr	Gly
		755					760					765			
Thr	Leu	Ser	Glu	Glu	Gln	Pro	Cys	Ser	Ser	Gly	Gln	Glu	Ala	Ile	Leu
	770					775					780				
Gly	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Pro	Glu	Arg	Met
785					790					795					800
Ile	Leu	Gly	Lys	Glu	Gly	Thr	Thr	Leu	Glu	Pro	Glu	Glu	Gln	Arg	Ile
			805						810					815	
Leu	Gly	Glu	Glu	Met	Gly	Thr	Phe	Ser	Ser	Ser	Pro	Gln	Lys	His	Arg
			820					825					830		
Ser	Leu	Val	Asn	Glu	Glu	Asp	Trp	Asp	Ile	Ser	Lys	Glu	Met	Lys	Glu
		835					840					845			
Ser	Arg	Val	Pro	Ser	Leu	Ala	Ser	Gln	Glu	Arg	Asn	Ile	Ile	Gly	Gln
	850					855					860				
Glu	Glu	Ala	Gly	Ala	Trp	Asn	Leu	Trp	Glu	Lys	Glu	His	Gly	Asn	Leu
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09686346 101000

55

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<213> Homo sapien
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<400> 5


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<211> 314
<212> DNA
<213> Homo sapien
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<213> Homo sapien
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tgcctttcca	ataggttctt	tattctctcg	ctgcgttcct	tctgaagggc	agccagctcc		120
tcttcaatct	tctgctcaag	gtgtgggtctg	cgcagagaca	ctctctgctc	tagctttctgg		180
agctcacgtt	catgttggtg	ctctgttngn	atcttgattt	ggntctggta	ggcgttgagc		240
agctccattt	cctgctggag	ctgtagcctc	aaggcctggc	attctgcttc	ttgagcctca		300
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aaaatggcaa							370

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aagaatgagc acaaaaacaat cttaaagaca ctgaaagatg agcagacaag aaaacttgcc     180  
attttggcag                                     190
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gctca

65

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 <212> DNA
 <213> Homo sapien

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 <223> N = a, c, t, g

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 atctgatccg ttctacagcac cagacgggaa tggaaaacca gctggagtag aataagaggc 120
 gagaaagaga actgcacaga aagcatgtca tggaaacttcg gcaacagcca aaaaacttaa 180
 aggccatgga antgcaattt aaaaaacagt tccaggaaa 219

<210> 11
 <211> 85
 <212> DNA
 <213> Homo sapien

<220>
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 <222> (1)...(85)
 <223> N = a, c, t, g

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 gatgtcatag tacttggctg ccggg 85

<210> 12
 <211> 46
 <212> DNA
 <213> Homo sapien

<400> 12
 ctccattggg tactacagtg tggagagctga gtgcatatgg tatatt 46

<210> 13
 <211> 116
 <212> DNA
 <213> Homo sapien

<400> 13
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 agtatgaatg caatgtctgc cctctaccat attgctcaaa atgacctcc aactct 116

<210> 14
 <211> 118
 <212> DNA
 <213> Homo sapien

<400> 14
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 aacgtgctgc tctcgagca gggatgatgtg aagatggcag acttcggtgt ggctggca 118

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 <212> DNA
 <213> Homo sapien

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<210> 16
 <211> 134
 <212> DNA
 <213> Homo sapien

<400> 16
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 cagatatcaa cttt 134

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 <212> PRT
 <213> Saccharomyces cerevisiae

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 20 25 30
 Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr Asp Lys Lys
 35 40 45
 Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser Gly Lys Gln
 50 55 60
 Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser Phe Leu Asn
 65 70 75 80
 Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys Phe Leu Lys
 85 90 95
 Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly Ser Ala Ala
 100 105 110
 Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val Glu Ile Ala
 115 120 125
 Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu His Ser Leu
 130 135 140
 Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Ser Asp
 145 150 155 160
 His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Leu Val Asp
 165 170 175
 Pro Ala Gln Thr Phe Ile Gly Thr Pro Phe Phe Met Ala Pro Glu Val
 180 185 190
 Ile Leu Ala Met Asp Glu Gly His Tyr Thr Asp Arg Ala Asp Ile Trp
 195 200 205
 Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Pro Pro Leu
 210 215 220
 Phe Ser Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp
 225 230 235 240
 Pro Pro Thr Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro Glu Trp Ser
 245 250 255
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270

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Lys	Ile	Gly 35	Gln	Gly	Ala	Ser	Gly 40	Gly	Val	Tyr	Thr	Ala 45	Tyr	Glu	Ile
Gly	Thr 50	Asn	Val	Ser	Val	Ala 55	Ile	Lys	Gln	Met	Asn 60	Leu	Glu	Lys	Gln
Pro 65	Lys	Lys	Glu	Leu	Ile 70	Ile	Asn	Glu	Ile	Leu 75	Val	Met	Lys	Gly	Ser 80
Lys	His	Pro	Asn 85	Ile	Val	Asn	Phe	Ile	Asp 90	Ser	Tyr	Val	Leu 95	Lys	Gly
Asp	Leu	Trp	Val 100	Ile	Met	Glu	Tyr	Met 105	Glu	Gly	Gly	Ser	Leu 110	Thr	Val
Asp	Val	Val 115	Thr	His	Cys	Ile	Leu 120	Thr	Glu	Gly	Gln	Ile 125	Gly	Ala	Val
Cys	Arg 130	Glu	Thr	Leu	Ser	Gly 135	Leu	Glu	Phe	Leu	His 140	Ser	Lys	Gly	Val
Leu 145	His	Arg	Asp	Ile	Lys 150	Ser	Asp	Asn	Ile	Leu 155	Leu	Ser	Met	Glu	Gly 160
Asp	Ile	Lys	Leu 165	Thr	Asp	Phe	Gly	Phe 170	Cys	Ala	Gln	Ile	Asn 175	Glu	Leu
Asn	Leu	Lys 180	Arg	Thr	Thr	Met	Val	Gly 185	Thr	Pro	Tyr	Trp	Met 190	Ala	Pro
Glu	Val	Val 195	Ser	Arg	Lys	Glu	Tyr 200	Gly	Pro	Lys	Val	Asp 205	Ile	Trp	Ser
Leu 210	Gly	Ile	Met	Ile	Ile	Glu 215	Met	Ile	Glu	Gly	Glu	Pro	Pro	Tyr	Leu
Asn 225	Glu	Thr	Pro	Leu	Arg 230	Ala	Leu	Tyr	Leu	Ile	Ala	Thr	Asn	Gly	Thr 240
Pro	Lys	Leu	Lys 245	Glu	Pro	Glu	Asn	Leu	Ser 250	Ser	Ser	Ser	Leu	Lys	Phe 255
Leu	Asp	Trp	Cys 260	Leu	Cys	Cys	Val	Glu 265	Pro	Glu	Asp	Arg	Ala	Ser	Ala
Thr															

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<222> (1)...(33)
<223> N = inosineI

<223> Oligonucleotide primers
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60

33

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<220>
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<223> N = inosineI
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21

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28

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30

61

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aaa tgg aat gat att ctt aaa gaa gtg tct ttt ctg aat aca gtt gtt Lys Trp Asn Asp Ile Leu Lys Glu Val Ser Phe Leu Asn Thr Val Val 75 80 85	536
cat cca cat att gtc gac tac aag gct tgt ttt ctt aag gac act aca His Pro His Ile Val Asp Tyr Lys Ala Cys Phe Leu Lys Asp Thr Thr 90 95 100	584
tgt tgg ctt gtg atg gag tac tgt att ggc tct gca gcc gat ata gtg Cys Trp Leu Val Met Glu Tyr Cys Ile Gly Ser Ala Ala Asp Ile Val 105 110 115	632
gat gtc ttg cga aaa gga atg cga gaa gtc gaa atc gct gcg att tgc Asp Val Leu Arg Lys Gly Met Arg Glu Val Glu Ile Ala Ala Ile Cys 120 125 130	680
tct caa act ttg gat gct ctt cga tat ctt cac tct ctg aag cga ata Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu His Ser Leu Lys Arg Ile 135 140 145 150	728
cat cga gat att aaa gct gga aat att ctg cta tct gat cat gct att His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Ser Asp His Ala Ile 155 160 165	776
gtt aaa cta gct gat ttc gga tcc gca tcc ctg gta gat ccg gct caa Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Leu Val Asp Pro Ala Gln 170 175 180	824
act ttc atc gga acg ccg ttt ttc atg gcc cca gag gta att ctg gca Thr Phe Ile Gly Thr Pro Phe Phe Met Ala Pro Glu Val Ile Leu Ala 185 190 195	872
atg gat gag ggt cac tac acg gat cgt gca gat att tgg tca ttg ggt Met Asp Glu Gly His Tyr Thr Asp Arg Ala Asp Ile Trp Ser Leu Gly 200 205 210	920
atc acg tgt ata gag ctg gcc gaa cgt cgt cca cca ttg ttc agt atg Ile Thr Cys Ile Glu Leu Ala Glu Arg Arg Pro Pro Leu Phe Ser Met 215 220 225 230	968
aat gca atg tct gcc ctc tac cat att gct caa aat gat cct cca act Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn Asp Pro Pro Thr 235 240 245	1016
ctt tct cca att gac act agc gaa caa ccg gaa tgg tcg ctg gaa ttc Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro Glu Trp Ser Leu Glu Phe 250 255 260	1064
gtt caa ttt ata gac aaa tgt ctt cga aaa cca gca gaa gag cga atg	1112

Val	Gln	Phe	Ile	Asp	Lys	Cys	Leu	Arg	Lys	Pro	Ala	Glu	Glu	Arg	Met	
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Ser	Ala	Glu	Glu	Cys	Phe	Arg	His	Pro	Phe	Ile	Gln	Arg	Ser	Arg	Pro	
	280					285					290					
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Ser	Asp	Thr	Ile	Gln	Glu	Leu	Ile	Gln	Arg	Thr	Lys	Asn	Met	Val	Leu	
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gag	ttg	gat	aat	ttt	caa	tac	aaa	aag	atg	aga	aaa	ctc	atg	tat	ttg	1256
Glu	Leu	Asp	Asn	Phe	Gln	Tyr	Lys	Lys	Met	Arg	Lys	Leu	Met	Tyr	Leu	
				315					320					325		
gat	gaa	aca	gaa	gga	aaa	gaa	gga	agt	gaa	gga	aat	gga	gca	tct	gat	1304
Asp	Glu	Thr		Gly	Lys	Glu	Gly	Ser	Glu	Gly	Asn	Gly	Ala	Ser	Asp	
			330					335					340			
gat	tta	gat	ttt	cat	gga	aat	gaa	gct	aat	tca	att	gga	aga	gca	gga	1352
Asp	Leu	Asp	Phe	His	Gly	Asn	Glu	Ala	Asn	Ser	Ile	Gly	Arg	Ala	Gly	
			345				350					355				
gat	tct	gcg	tca	tct	cga	agt	gct	tct	ctt	act	tct	ttc	cga	tca	atg	1400
Asp	Ser	Ala	Ser	Ser	Arg	Ser	Ala	Ser	Leu	Thr	Ser	Phe	Arg	Ser	Met	
	360					365					370					
cag	agt	agt	gga	gga	gct	ggt	ctt	tta	gtg	tcc	acc	aat	acg	acg	ggt	1448
Gln	Ser	Ser	Gly	Gly	Ala	Gly	Leu	Leu	Val	Ser	Thr	Asn	Thr	Thr	Gly	
	375				380					385					390	
gct	atg	gat	aat	gtg	cat	gga	tcc	tct	gga	tac	ggt	aat	gga	agt	agt	1496
Ala	Met	Asp	Asn	Val	His	Gly	Ser	Ser	Gly	Tyr	Gly	Asn	Gly	Ser	Ser	
				395					400					405		
tcg	acg	acg	agc	tcc	gca	cgc	cgc	cgt	cct	cca	att	cct	tcg	caa	atg	1544
Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Pro	Pro	Ile	Pro	Ser	Gln	Met	
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ctc	tct	tct	aca	tca	acg	tct	ggt	ggt	gga	act	atg	ccg	agt	cat	gga	1592
Leu	Ser	Ser	Thr	Ser	Thr	Ser	Gly	Val	Gly	Thr	Met	Pro	Ser	His	Gly	
			425				430					435				
tca	gtt	gga	gca	tcg	att	acg	gcg	atc	gca	gtc	aat	cca	aca	ccg	tct	1640
Ser	Val	Gly	Ala	Ser	Ile	Thr	Ala	Ile	Ala	Val	Asn	Pro	Thr	Pro	Ser	
	440					445					450					
cct	tca	gaa	cct	atc	cca	aca	tca	caa	cca	aca	tcg	aaa	tca	gaa	tca	1688
Pro	Ser	Glu	Pro	Ile	Pro	Thr	Ser	Gln	Pro	Thr	Ser	Lys	Ser	Glu	Ser	
	455				460					465					470	
tct	tct	ata	ctc	gaa	act	gca	cac	gat	gat	cct	ttg	gac	acg	tcg	ata	1736
Ser	Ser	Ile	Leu	Glu	Thr	Ala	His	Asp	Asp	Pro	Leu	Asp	Thr	Ser	Ile	
				475					480					485		
cgt	gct	cca	gtg	aaa	gac	ttg	cat	atg	ccg	cat	cga	gca	gtc	aag	gaa	1784
Arg	Ala	Pro	Val	Lys	Asp	Leu	His	Met	Pro	His	Arg	Ala	Val	Lys	Glu	
			490					495					500			

65

Lys	Gln	His	Glu	Met	Thr	Arg	Asp	Leu	Glu	Ile	Gln	His	Leu	Asn	Glu		
			730					735					740				
ctt	cac	gcg	atg	aaa	aaa	cga	cat	ttg	gag	aca	caa	cac	gag	gcg	gaa	2552	
Leu	His	Ala	Met	Lys	Lys	Arg	His	Leu	Glu	Thr	Gln	His	Glu	Ala	Glu		
		745					750					755					
tcg	gca	agt	caa	aat	gag	tac	aca	cag	agg	caa	cag	gat	gaa	ttg	aga	2600	
Ser	Ala	Ser	Gln	Asn	Glu	Tyr	Thr	Gln	Arg	Gln	Gln	Asp	Glu	Leu	Arg		
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aaa	aag	cat	gcg	atg	cag	tca	aga	caa	cag	cca	aga	gat	tta	aag	atc	2648	
Lys	Lys	His	Ala	Met	Gln	Ser	Arg	Gln	Gln	Pro	Arg	Asp	Leu	Lys	Ile		
775					780					785					790		
caa	gaa	gca	caa	att	cga	aaa	caa	tac	cga	caa	gtt	gtg	aag	act	cag	2696	
Gln	Glu	Ala	Gln	Ile	Arg	Lys	Gln	Tyr	Arg	Gln	Val	Val	Lys	Thr	Gln		
			795						800					805			
act	cgc	caa	ttt	aag	ctc	tac	ctt	aca	caa	atg	gtg	caa	gta	gtt	cca	2744	
Thr	Arg	Gln	Phe	Lys	Leu	Tyr	Leu	Thr	Gln	Met	Val	Gln	Val	Val	Pro		
			810					815					820				
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Lys	Asp	Glu	Gln	Lys	Glu	Leu	Thr	Ser	Arg	Leu	Lys	Gln	Asp	Gln	Met		
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Met	Val	Gln	Asp	Lys	Thr	Val	Lys	Leu	Glu	Ser	Trp	Gln	Glu	Asp	Glu		
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Gln	Arg	Val	Leu	Ser	Glu	Lys	Leu	Glu	Lys	Glu	Leu	Glu	Glu	Leu	Ile		
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gct	tat	cag	aag	aag	acg	aga	gcc	aca	tta	gaa	gag	cag	att	aaa	aag	2984	
Ala	Tyr	Gln	Lys	Lys	Thr	Arg	Ala	Thr	Leu	Glu	Glu	Gln	Ile	Lys	Lys		
			890					895					900				
gaa	cgt	acg	gca	ctc	gaa	gaa	cga	att	ggc	aca	cga	cgt	gca	atg	ctt	3032	
Glu	Arg	Thr	Ala	Leu	Glu	Glu	Arg	Ile	Gly	Thr	Arg	Arg	Ala	Met	Leu		
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gaa	cag	aag	att	att	gaa	gaa	cgc	gaa	caa	atg	gga	gaa	atg	cgt	cga	3080	
Glu	Gln	Lys	Ile	Ile	Glu	Glu	Arg	Glu	Gln	Met	Gly	Glu	Met	Arg	Arg		
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cta	aag	aag	gag	caa	atc	cgt	gat	cga	cac	agt	caa	gaa	cgc	cat	cgt	3128	
Leu	Lys	Lys	Glu	Gln	Ile	Arg	Asp	Arg	His	Ser	Gln	Glu	Arg	His	Arg		
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ctc	gag	aat	cat	ttc	gta	cgg	acg	ggc	tcg	acg	agc	aga	agt	tct	gg	3176	
Leu	Glu	Asn	His	Phe	Val	Arg	Thr	Gly	Ser	Thr	Ser	Arg	Ser	Ser	Gly		
				955					960					965			

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 35 40 45
 Asp Lys Lys Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser
 50 55 60
 Gly Lys Gln Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser
 65 70 75 80
 Phe Leu Asn Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys
 85 90 95
 Phe Leu Lys Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly
 100 105 110
 Ser Ala Ala Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val
 115 120 125
 Glu Ile Ala Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu
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 His Ser Leu Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu
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 Leu Ser Asp His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser
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 Leu Val Asp Pro Ala Gln Thr Phe Ile Gly Thr Pro Phe Phe Met Ala
 180 185 190
 Pro Glu Val Ile Leu Ala Met Asp Glu Gly His Tyr Thr Asp Arg Ala
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 Asp Ile Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Arg
 210 215 220
 Pro Pro Leu Phe Ser Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala
 225 230 235 240
 Gln Asn Asp Pro Pro Thr Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro
 245 250 255
 Glu Trp Ser Leu Glu Phe Val Gln Phe Ile Asp Lys Cys Leu Arg Lys

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Ile Gln His Leu Asn Glu Leu His Ala Met Lys Lys Arg His Leu Glu
 725 740 745 750
 Thr Gln His Glu Ala Glu Ser Ala Ser Gln Asn Glu Tyr Thr Gln Arg
 755 760 765
 Gln Gln Asp Glu Leu Arg Lys Lys His Ala Met Gln Ser Arg Gln Gln
 770 775 780
 Pro Arg Asp Leu Lys Ile Gln Glu Ala Gln Ile Arg Lys Gln Tyr Arg
 785 790 795 800
 Gln Val Val Lys Thr Gln Thr Arg Gln Phe Lys Leu Tyr Leu Thr Gln
 805 810 815
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